

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/530,106
Source: PUT/10
Date Processed by STIC: 4/12/05

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/530,106

DATE: 04/12/2005
TIME: 10:20:31

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\04122005\J530106.raw

5 <110> APPLICANT: Hooft Van Huijsdijnen, Rob
 6 Walchli, Sebastien
 9 <120> TITLE OF INVENTION: Use of protein tyrosine phosphatase inhibitors for prevention and/or
 10 treatment of cancer
 14 <130> FILE REFERENCE: SLII-P01-003
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/530,106
 C--> 17 <141> CURRENT FILING DATE: 2005-04-01
 17 <160> NUMBER OF SEQ ID NOS: 34
 21 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 27 <211> LENGTH: 1115
 29 <212> TYPE: PRT
 31 <213> ORGANISM: Homo sapiens
 35 <400> SEQUENCE: 1
 37 Met Ala Gly Ala Gly Gly Gly Leu Gly Val Trp Gly Asn Leu Val Leu
 38 1 5 10 15
 41 Leu Gly Leu Cys Ser Trp Thr Gly Ala Arg Ala Pro Ala Pro Asn Pro
 42 20 25 30
 45 Gly Arg Asn Leu Thr Val Glu Thr Gln Thr Thr Ser Ser Ile Ser Leu
 46 35 40 45
 49 Ser Trp Glu Val Pro Asp Gly Leu Asp Ser Gln Asn Ser Asn Tyr Trp
 50 50 55 60
 53 Val Gln Cys Thr Gly Asp Gly Gly Thr Thr Glu Thr Arg Asn Thr Thr
 54 65 70 75 80
 57 Ala Thr Asn Val Thr Val Asp Gly Leu Gly Pro Gly Ser Leu Tyr Thr
 58 85 90 95
 61 Cys Ser Val Trp Val Glu Lys Asp Gly Val Asn Ser Ser Val Gly Thr
 62 100 105 110
 65 Val Thr Thr Ala Thr Ala Pro Asn Pro Val Arg Asn Leu Arg Val Glu
 .66 115 120 125
 69 Ala Gln Thr Asn Ser Ser Ile Ala Leu Thr Trp Glu Val Pro Asp Gly
 70 130 135 140
 73 Pro Asp Pro Gln Asn Ser Thr Tyr Gly Val Glu Tyr Thr Gly Asp Gly
 74 145 150 155 160
 77 Gly Arg Ala Gly Thr Arg Ser Thr Ala His Thr Asn Ile Thr Val Asp
 78 165 170 175
 81 Gly Leu Glu Pro Gly Cys Leu Tyr Ala Phe Ser Met Trp Val Gly Lys
 82 180 185 190
 85 Asn Gly Ile Asn Ser Ser Arg Glu Thr Arg Asn Ala Thr Thr Ala His
 86 195 200 205
 89 Asn Pro Val Arg Asn Leu Arg Val Glu Ala Gln Thr Thr Ser Ser Ile
 90 210 215 220
 93 Ser Leu Ser Trp Glu Val Pro Asp Gly Thr Asp Pro Gln Asn Ser Thr

*Does Not Comply
Rejected Diskette Needed*

Jpp 6-7

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Input Set : A:\pto.da.txt
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94	225	230	235	240
97	Tyr Cys Ile Gln Cys Thr Gly Asp Gly Gly Arg Thr Glu Thr Arg Asn			
98	245	250	255	
101	Thr Thr Asp Thr Arg Val Thr Val Asp Gly Leu Gly Pro Gly Ser Leu			
102	260	265	270	
105	Tyr Thr Cys Ser Val Trp Val Glu Lys Asp Gly Val Asn Ser Ser Val			
106	275	280	285	
109	Glu Ile Val Thr Ser Thr Ala Pro Asn Pro Val Arg Asn Leu Thr			
110	290	295	300	
113	Val Glu Ala Gln Thr Asn Ser Ser Ile Ala Leu Thr Trp Glu Val Pro			
114	305	310	315	320
117	Asp Gly Pro Asp Pro Gln Asn Ser Thr Tyr Gly Val Glu Tyr Thr Gly			
118	325	330	335	
121	Asp Gly Gly Arg Ala Gly Thr Arg Ser Thr Ala His Thr Asn Ile Thr			
122	340	345	350	
125	Val Asp Arg Leu Glu Pro Gly Cys Leu Tyr Val Phe Ser Val Trp Val			
126	355	360	365	
131	Gly Lys Asn Gly Ile Asn Ser Ser Arg Glu Thr Arg Asn Ala Thr Thr			
132	370	375	380	
135	Ala Pro Asn Pro Val Arg Asn Leu His Met Glu Thr Gln Thr Asn Ser			
136	385	390	395	400
139	Ser Ile Ala Leu Cys Trp Glu Val Pro Asp Gly Pro Tyr Pro Gln Asp			
140	405	410	415	
143	Tyr Thr Tyr Trp Val Glu Tyr Thr Gly Asp Gly Gly Thr Glu Thr			
144	420	425	430	
147	Arg Asn Thr Thr Asn Thr Ser Val Thr Ala Glu Arg Leu Glu Pro Gly			
148	435	440	445	
151	Thr Leu Tyr Thr Phe Ser Val Trp Ala Glu Lys Asn Gly Ala Arg Gly			
152	450	455	460	
155	Ser Arg Gln Asn Val Ser Ile Ser Thr Val Pro Asn Ala Val Thr Ser			
156	465	470	475	480
159	Leu Ser Lys Gln Asp Trp Thr Asn Ser Thr Ile Ala Leu Arg Trp Thr			
160	485	490	495	
163	Ala Pro Gln Gly Pro Gly Gln Ser Ser Tyr Ser Tyr Trp Val Ser Trp			
164	500	505	510	
167	Val Arg Glu Gly Met Thr Asp Pro Arg Thr Gln Ser Thr Ser Gly Thr			
168	515	520	525	
171	Asp Ile Thr Leu Lys Glu Leu Glu Ala Gly Ser Leu Tyr His Leu Thr			
172	530	535	540	
175	Val Trp Ala Glu Arg Asn Glu Val Arg Gly Tyr Asn Ser Thr Leu Thr			
176	545	550	555	560
179	Ala Ala Thr Ala Pro Asn Glu Val Thr Asp Leu Gln Asn Glu Thr Gln			
180	565	570	575	
183	Thr Lys Asn Ser Val Met Leu Trp Trp Lys Ala Pro Gly Asp Pro His			
184	580	585	590	
187	Ser Gln Leu Tyr Val Tyr Trp Val Gln Trp Ala Ser Lys Gly His Pro			
188	595	600	605	
191	Arg Arg Gly Gln Asp Pro Gln Ala Asn Trp Val Asn Gln Thr Ser Arg			
192	610	615	620	

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195 Thr Asn Glu Thr Trp Tyr Lys Val Glu Ala Leu Glu Pro Gly Thr Leu
 196 625 630 635 640
 199 Tyr Asn Phe Thr Val Trp Ala Glu Arg Asn Asp Val Ala Ser Ser Thr
 200 645 650 655
 203 Gln Ser Leu Cys Ala Ser Thr Tyr Pro Asp Thr Val Thr Ile Thr Ser
 204 660 665 670
 207 Cys Val Ser Thr Ser Ala Gly Tyr Gly Val Asn Leu Ile Trp Ser Cys
 208 675 680 685
 211 Pro Gln Gly Gly Tyr Glu Ala Phe Glu Leu Glu Val Gly Gly Gln Arg
 212 690 695 700
 215 Gly Ser Gln Asp Arg Ser Ser Cys Gly Glu Ala Val Ser Val Leu Gly
 216 705 710 715 720
 219 Leu Gly Pro Ala Arg Ser Tyr Pro Ala Thr Ile Thr Thr Ile Trp Asp
 220 725 730 735
 223 Gly Met Lys Val Val Ser His Ser Val Val Cys His Thr Glu Ser Ala
 224 740 745 750
 227 Gly Val Ile Ala Gly Ala Phe Val Gly Ile Leu Leu Phe Leu Ile Leu
 228 755 760 765
 231 Val Gly Leu Leu Ile Phe Phe Leu Lys Arg Arg Asn Lys Lys Lys Gln
 232 770 775 780
 235 Gln Lys Pro Glu Leu Arg Asp Leu Val Phe Ser Ser Pro Gly Asp Ile
 236 785 790 795 800
 239 Pro Ala Glu Asp Phe Ala Asp His Val Arg Lys Asn Glu Arg Asp Ser
 240 805 810 815
 243 Asn Cys Gly Phe Ala Asp Glu Tyr Gln Gln Leu Ser Leu Val Gly His
 244 820 825 830
 247 Ser Gln Ser Gln Met Val Ala Ser Ala Ser Glu Asn Asn Ala Lys Asn
 248 835 840 845
 251 Arg Tyr Arg Asn Val Leu Pro Tyr Asp Trp Ser Arg Val Pro Leu Lys
 252 850 855 860
 255 Pro Ile His Glu Glu Pro Gly Ser Asp Tyr Ile Asn Ala Ser Phe Met
 256 865 870 875 880
 259 Pro Gly Leu Trp Ser Pro Gln Glu Phe Ile Ala Thr Gln Gly Pro Leu
 260 885 890 895
 263 Pro Gln Thr Val Gly Asp Phe Trp Arg Leu Val Trp Glu Gln Gln Ser
 264 900 905 910
 267 His Thr Leu Val Met Leu Thr Asn Cys Met Glu Ala Gly Arg Val Lys
 268 915 920 925
 271 Cys Glu His Tyr Trp Pro Leu Asp Ser Gln Pro Cys Thr His Gly His
 272 930 935 940
 275 Leu Arg Val Thr Leu Val Gly Glu Glu Val Met Glu Asn Trp Thr Val
 276 945 950 955 960
 279 Arg Glu Leu Leu Leu Gln Val Glu Glu Gln Lys Thr Leu Ser Val
 280 965 970 975
 283 Arg Gln Phe His Tyr Gln Ala Trp Pro Asp His Gly Val Pro Ser Ser
 284 980 985 990
 287 Pro Asp Thr Leu Leu Ala Phe Trp Arg Met Leu Arg Gln Trp Leu Asp
 288 995 1000 1005
 291 Gln Thr Met Glu Gly Gly Pro Pro Ile Val His Cys Ser Ala Gly

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Input Set : A:\pto.da.txt
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292	1010	1015	1020	
295	Val	Gly Arg Thr Gly Thr	Leu Ile Ala Leu Asp Val	Leu Leu Arg
296	1025		1030	1035
299	Gln	Leu Gln Ser Glu Gly	Leu Leu Gly Pro Phe Ser	Phe Val Arg
300	1040		1045	1050
303	Lys	Met Arg Glu Ser Arg	Pro Leu Met Val Gln Thr	Glu Ala Gln
304	1055		1060	1065
307	Tyr	Val Phe Leu His Gln	Cys Ile Leu Arg Phe Leu	Gln Gln Ser
308	1070		1075	1080
311	Ala	Gln Ala Pro Ala Glu	Lys Glu Val Pro Tyr Glu	Asp Val Glu
312	1085		1090	1095
315	Asn	Leu Ile Tyr Glu Asn Val	Ala Ala Ile Gln Ala	His Lys Leu
316	1100		1105	1110
319	Glu	Val		
320	1115			
323	<210>	SEQ ID NO: 2		
325	<211>	LENGTH: 20		
327	<212>	TYPE: DNA		
329	<213>	ORGANISM: Artificial Sequence		
333	<220>	FEATURE:		
335	<223>	OTHER INFORMATION: Primer		
337	<400>	SEQUENCE: 2		
338	ccagctcacc atggatgatg			20
341	<210>	SEQ ID NO: 3		
343	<211>	LENGTH: 22		
345	<212>	TYPE: DNA		
347	<213>	ORGANISM: Artificial Sequence		
351	<220>	FEATURE:		
353	<223>	OTHER INFORMATION: Primer		
355	<400>	SEQUENCE: 3		
356	ccttaatgtc acgcacgatt tc			22
359	<210>	SEQ ID NO: 4		
361	<211>	LENGTH: 20		
363	<212>	TYPE: DNA		
365	<213>	ORGANISM: Artificial Sequence		
369	<220>	FEATURE:		
371	<223>	OTHER INFORMATION: Primer		
373	<400>	SEQUENCE: 4		
374	catgctgacc aactgcatgg			20
377	<210>	SEQ ID NO: 5		
379	<211>	LENGTH: 20		
381	<212>	TYPE: DNA		
383	<213>	ORGANISM: Artificial Sequence		
387	<220>	FEATURE:		
389	<223>	OTHER INFORMATION: Primer		
391	<400>	SEQUENCE: 5		
392	gcgagtccag aggccagtaa			20
395	<210>	SEQ ID NO: 6		
397	<211>	LENGTH: 20		

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Input Set : A:\pto.da.txt
Output Set: N:\CRF4\04122005\J530106.raw

399 <212> TYPE: DNA
401 <213> ORGANISM: Artificial Sequence
405 <220> FEATURE:
407 <223> OTHER INFORMATION: Primer
409 <400> SEQUENCE: 6
410 gcgagtccag aggccagtaa 20
413 <210> SEQ ID NO: 7
415 <211> LENGTH: 20
417 <212> TYPE: DNA
419 <213> ORGANISM: Artificial Sequence
423 <220> FEATURE:
425 <223> OTHER INFORMATION: Primer
427 <400> SEQUENCE: 7
428 catgctgacc aactgcatgg 20
431 <210> SEQ ID NO: 8
433 <211> LENGTH: 22
435 <212> TYPE: DNA
437 <213> ORGANISM: Artificial Sequence
441 <220> FEATURE:
443 <223> OTHER INFORMATION: Primer
445 <400> SEQUENCE: 8
446 gatgggattt ccatttcatca ca 22
449 <210> SEQ ID NO: 9
451 <211> LENGTH: 18
453 <212> TYPE: DNA
455 <213> ORGANISM: Artificial Sequence
459 <220> FEATURE:
461 <223> OTHER INFORMATION: Primer
463 <400> SEQUENCE: 9
464 ccacccatgg caaattcc 18
467 <210> SEQ ID NO: 10
469 <211> LENGTH: 21
471 <212> TYPE: DNA
473 <213> ORGANISM: Artificial Sequence
477 <220> FEATURE:
479 <223> OTHER INFORMATION: Primer
481 <400> SEQUENCE: 10
482 ccttagtcccc gggctttgtat t 21
485 <210> SEQ ID NO: 11
487 <211> LENGTH: 22
489 <212> TYPE: DNA
491 <213> ORGANISM: Artificial Sequence
495 <220> FEATURE:
497 <223> OTHER INFORMATION: Primer
499 <400> SEQUENCE: 11
500 ctgtgctccc actcctgatt tc 22
503 <210> SEQ ID NO: 12
505 <211> LENGTH: 13
507 <212> TYPE: PRT

10/530, 106 6

<210> 32

<211> 20

<212> DNA

<213> Artificial sequence

needs explanation - see p. 7

<400> 32

gcgcgcgttagc cacttcggaa

20

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\pto.da.txt
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error explanation

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:32

7

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/530,106

DATE: 04/12/2005

TIME: 10:20:32

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\04122005\J530106.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:879 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial sequence
L:879 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial sequence
L:879 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32, Line#:879